

09875935.060801

A. Most strongly disease-associated patterns								
Marker	01	02	03	04	05	06	07	08
Pattern01	4	1	6	6	3	*	*	*
Pattern02	4	1	6	6	3	6	*	*
Pattern03	4	1	6	6	*	6	*	*
Pattern04	4	1	6	*	3	6	*	*
Pattern05	4	1	*	6	3	*	*	*
Pattern06	4	1	*	6	3	6	*	*
Pattern07	4	*	6	6	3	*	*	*
Pattern08	4	*	6	6	3	6	*	*
Pattern09	4	*	6	*	3	6	*	*
Pattern10	*	1	6	6	*	*	*	*
Pattern11	*	1	6	6	3	*	*	*

Frequency	9	11	11	11	10	6	0	0

FIG. 1A

B. Marker frequency histogram

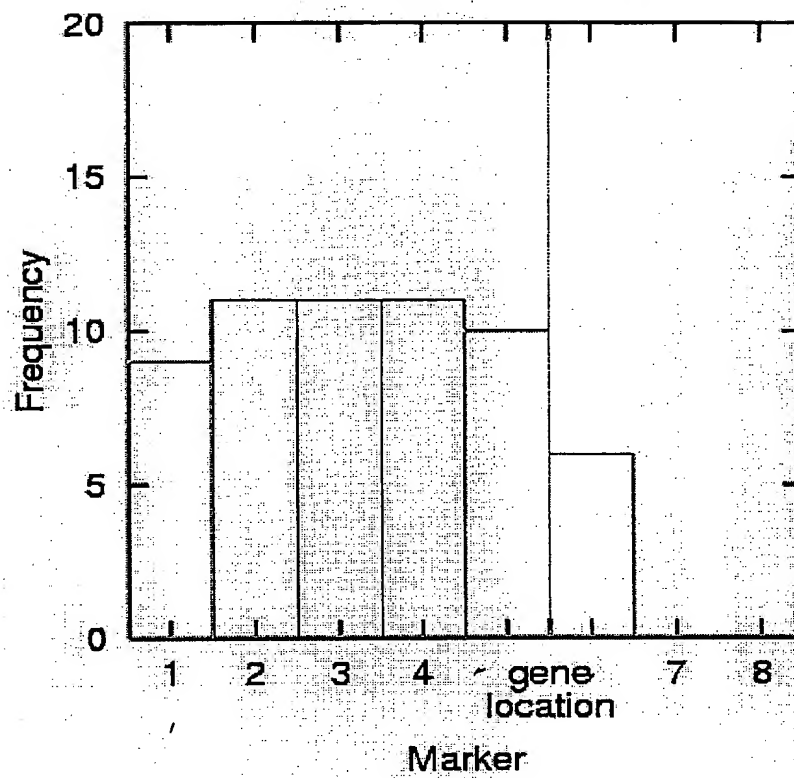


FIG 1B

C. Marker frequency histogram

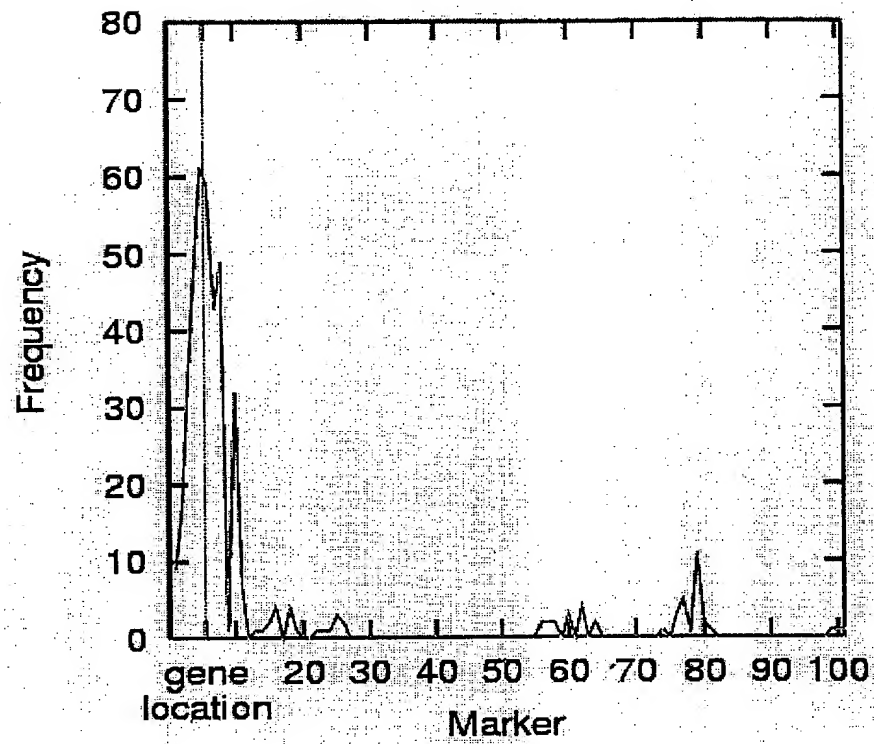


FIG. 1C

D. Prediction results (A = 10%)

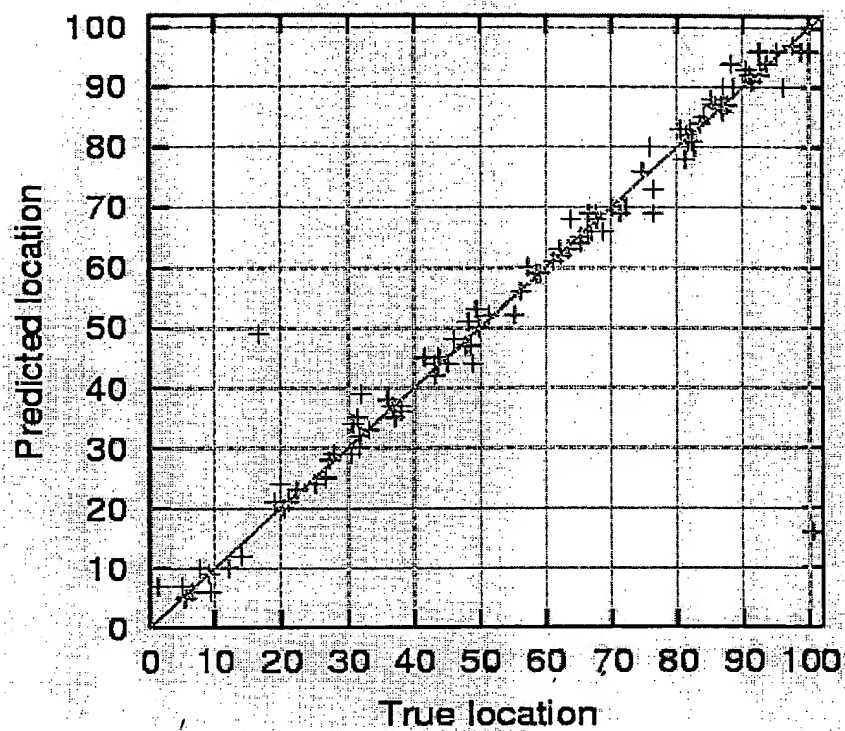


FIG. 1D

A. Influence of A

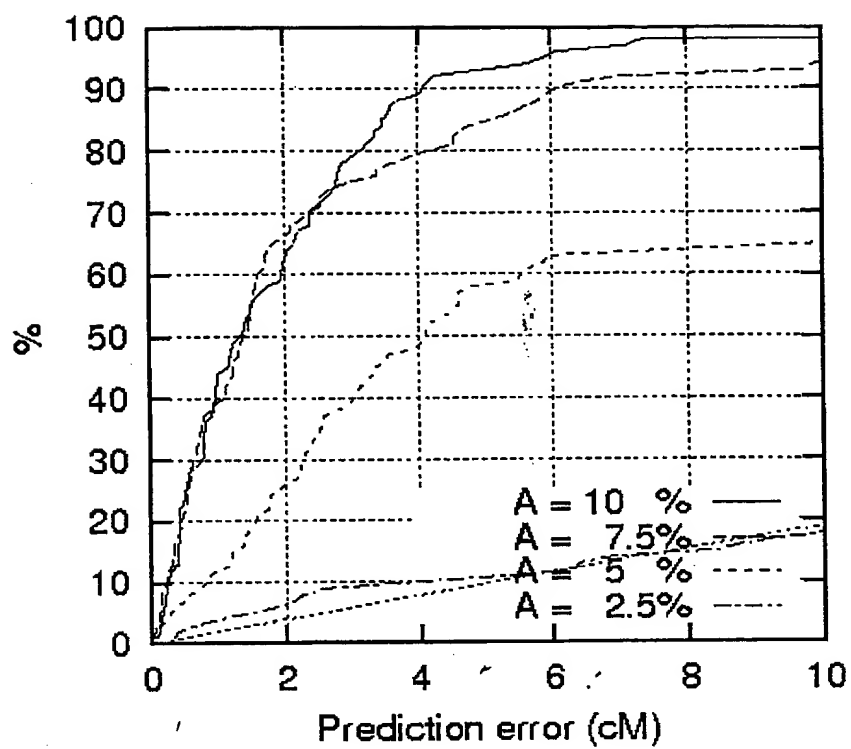


FIG. 2A

B. Influence of A (larger dataset)

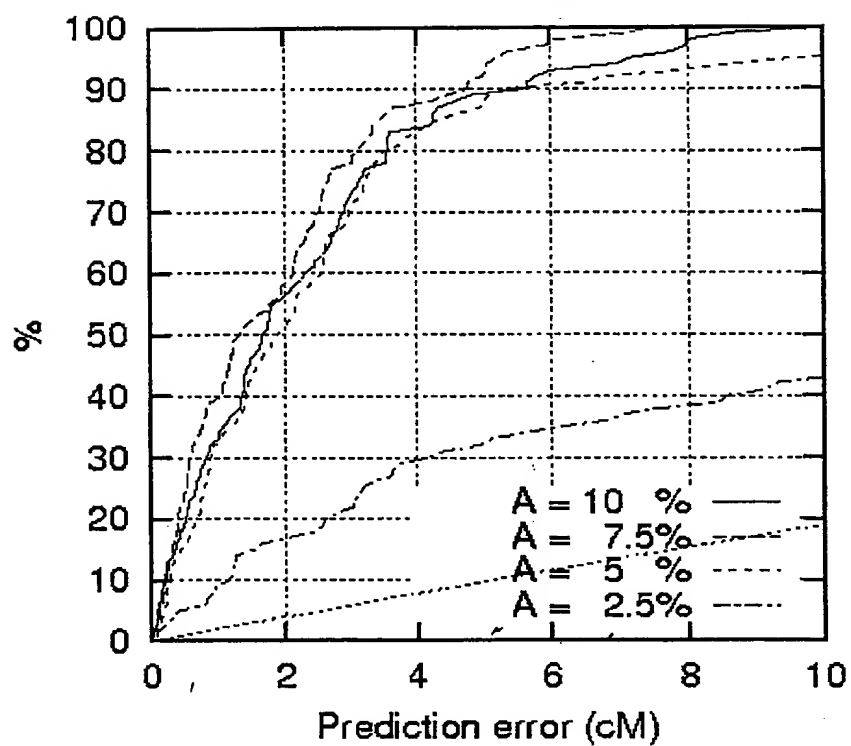


FIG. 2 B

C. Influence of corrupted data (A = 10%)

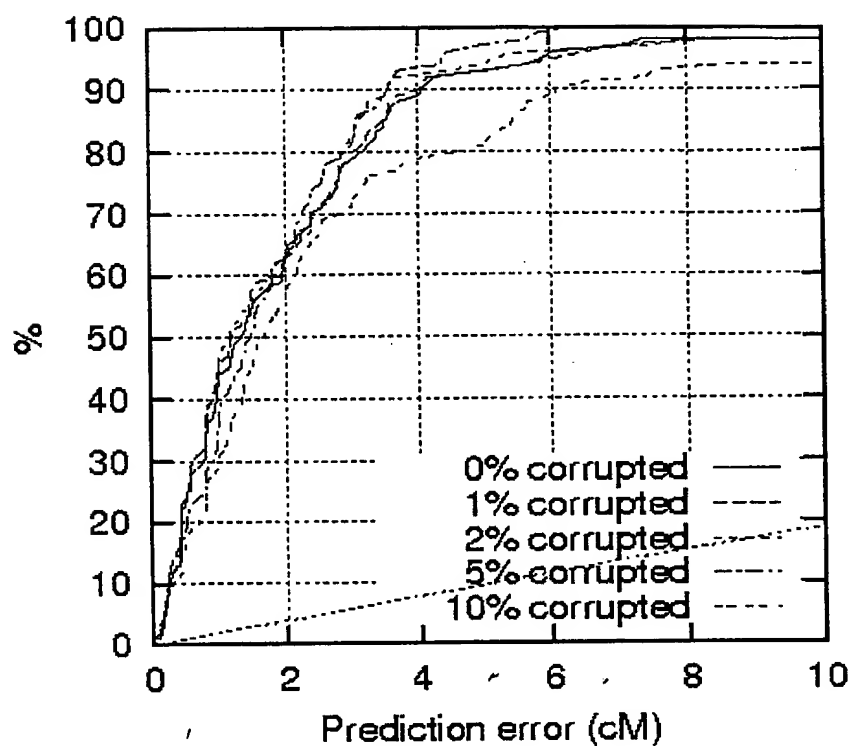


FIG. 2C

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D. Influence of missing data (A = 10%)

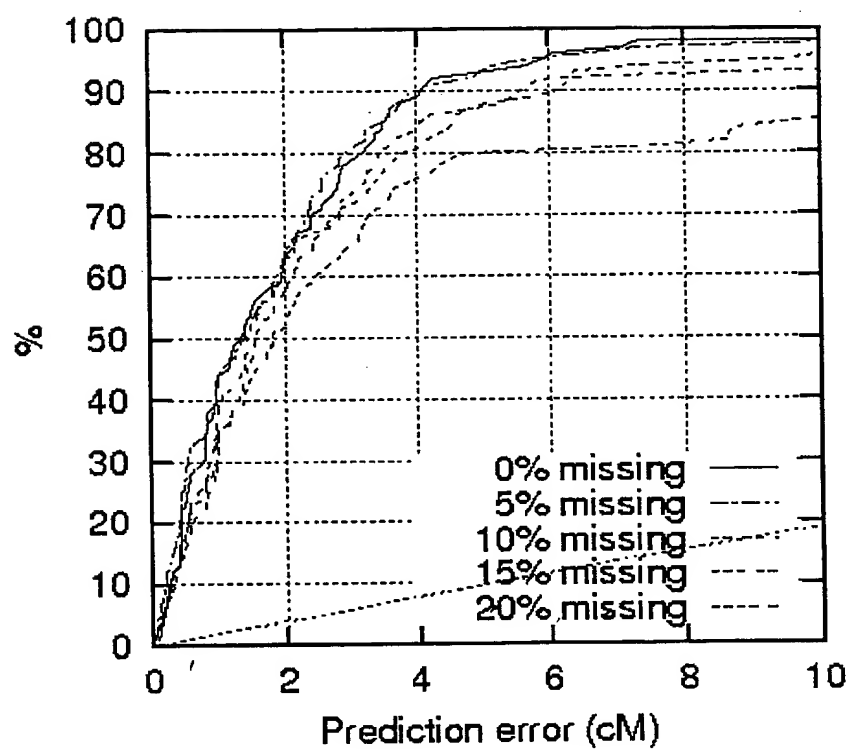


FIG. 2D

E. Comparison of prediction methods
(A = 10%, 0/1% corrupted, 0/20% missing)

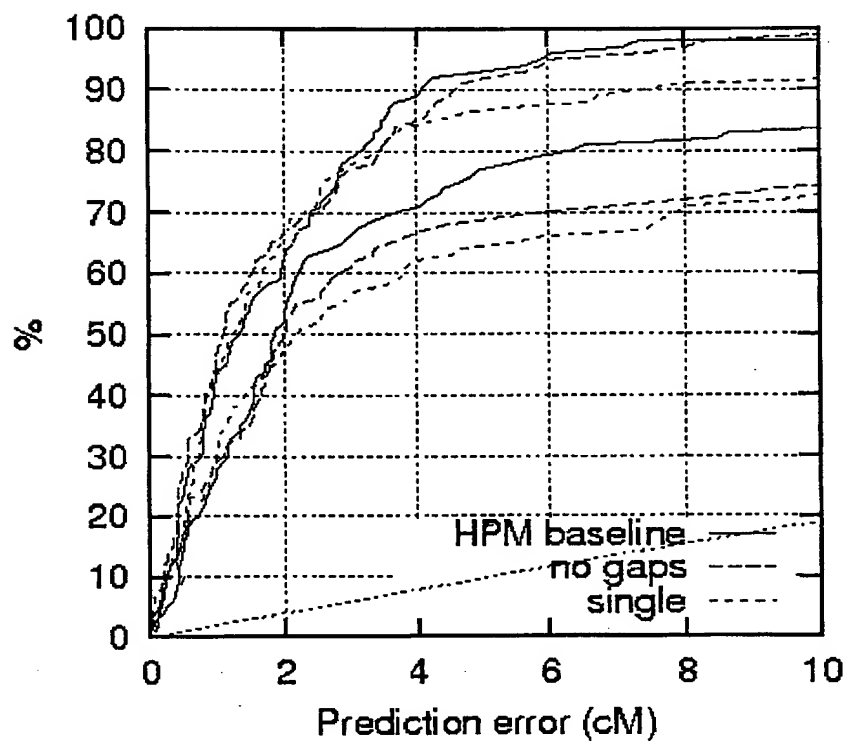


FIG. 2E

F. Influence of pattern parameters
(A = 10%, 1% corrupted, 20% missing)

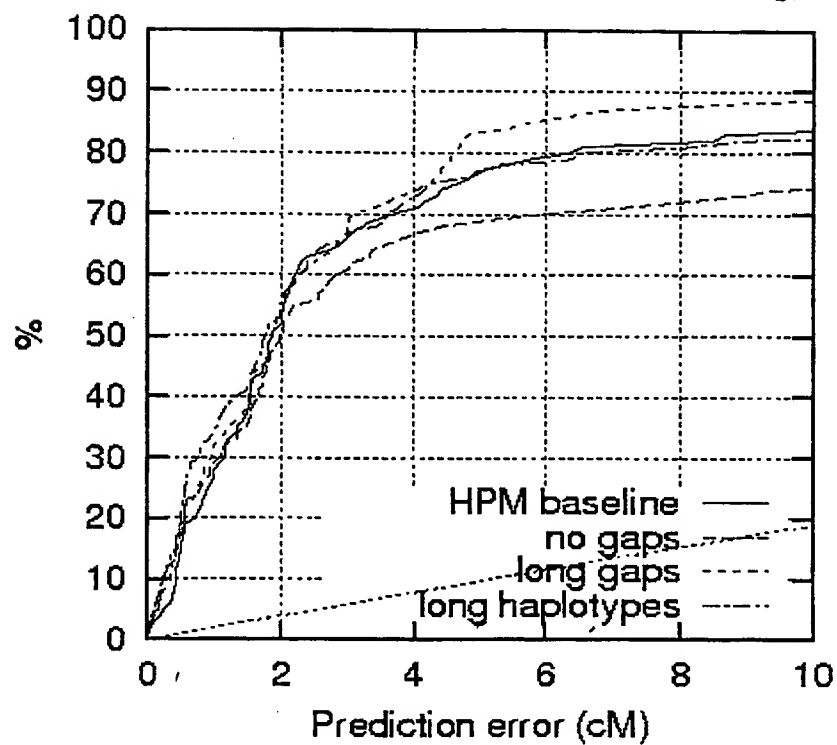


FIG. 2F

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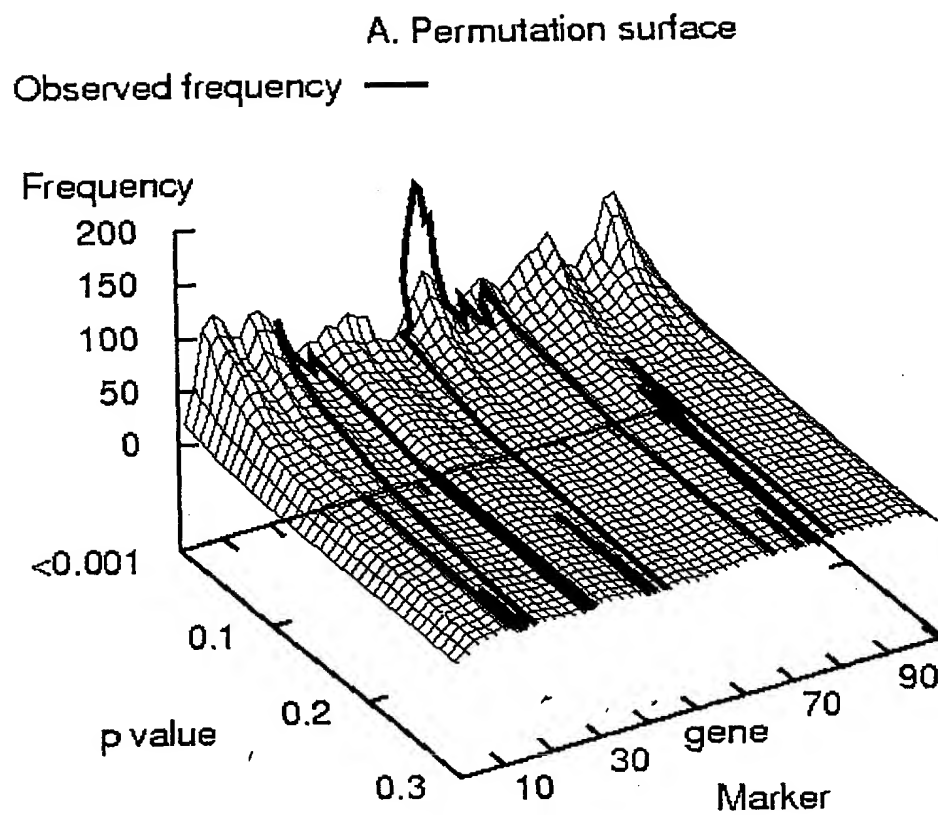


FIG. 3A

B. Marker-wise frequencies for some p values

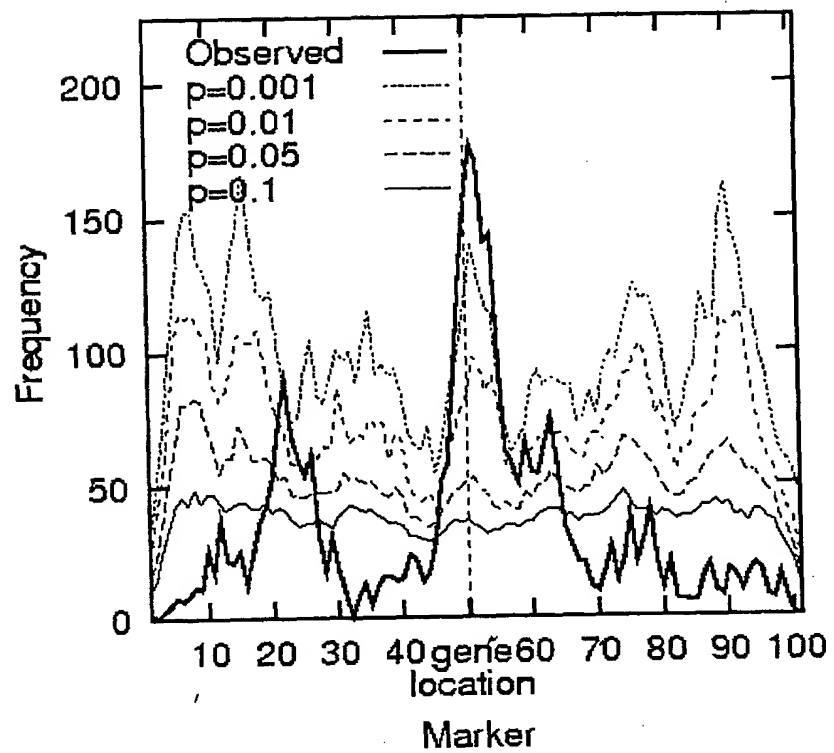


FIG. 3B

C. Marker-wise frequencies for some p values

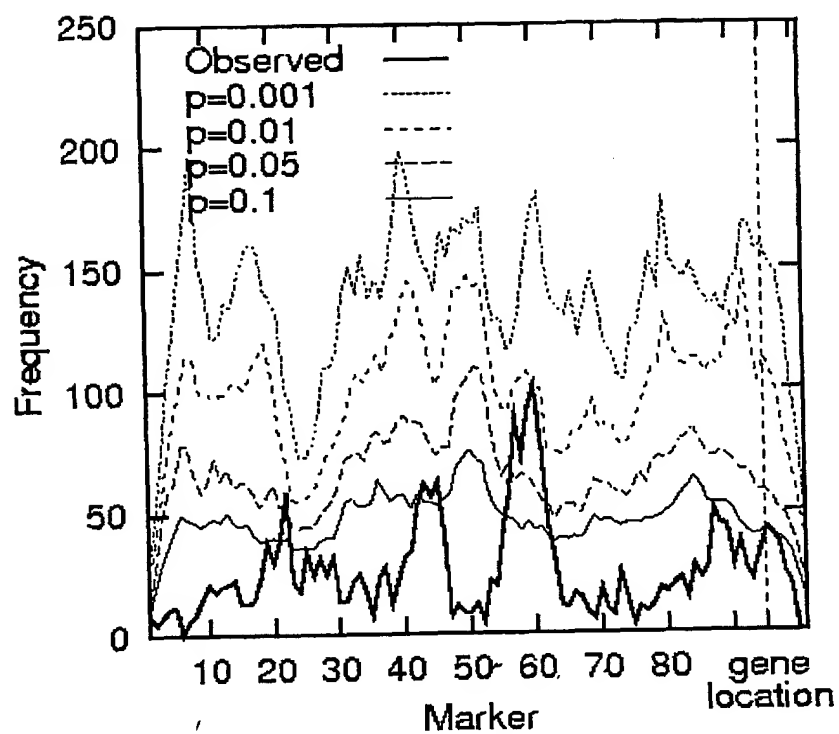


FIG. 3C

D. Influence of permutation tests ($A = 5\%$)

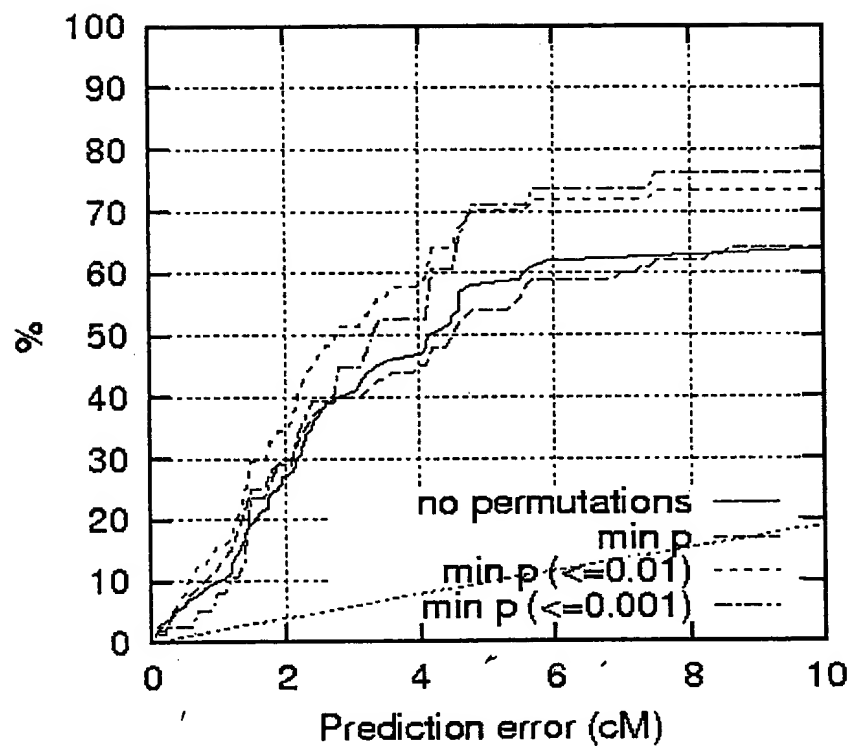


FIG. 3D

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Influence of A (SNP dataset, 12.5% missing data)

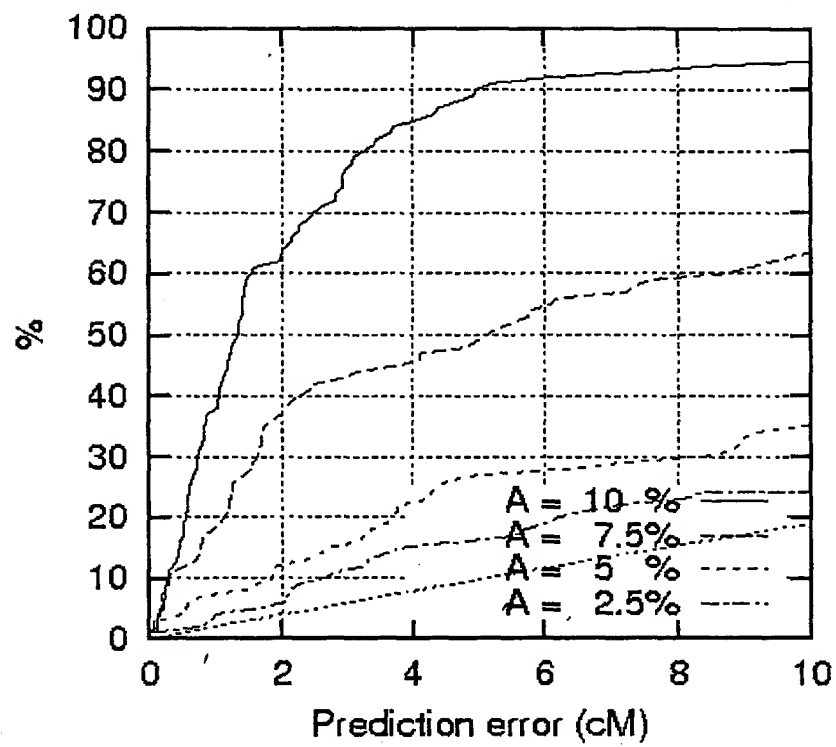


FIG. 4

A. Marker frequencies in HLA data

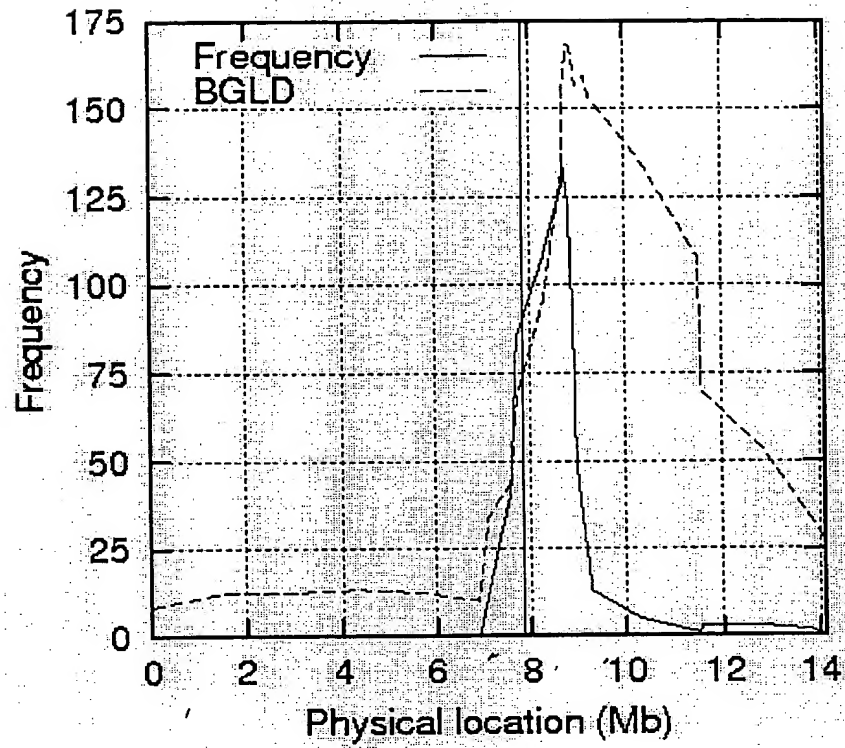


FIG. 5A

B. P values and frequency ratios in HLA data

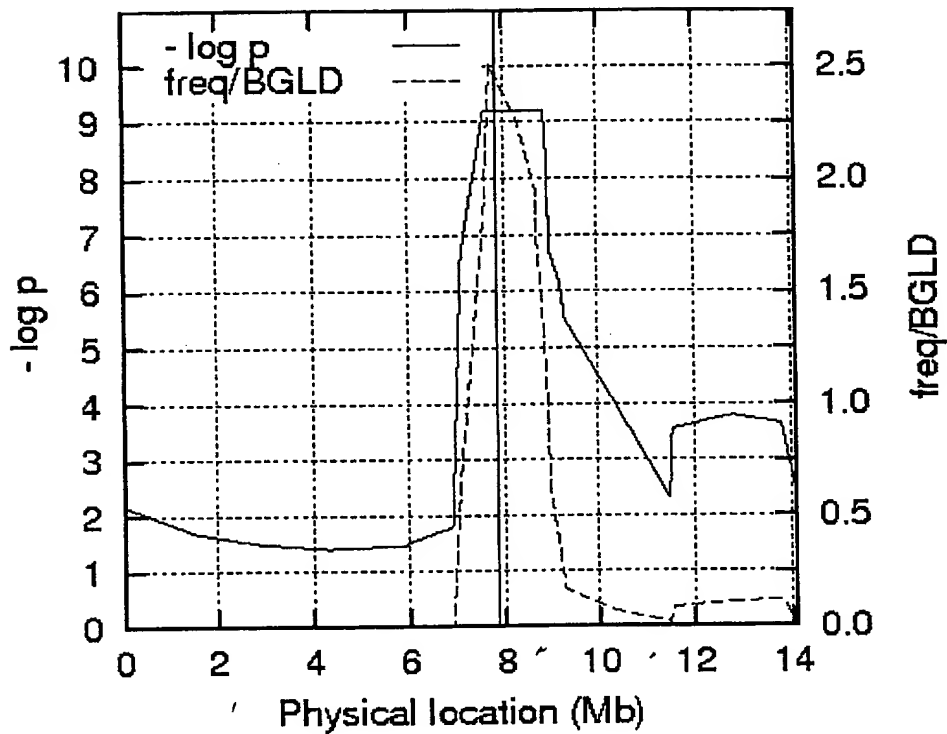


FIG. 5B

A. Marker frequency histogram (2 genes)

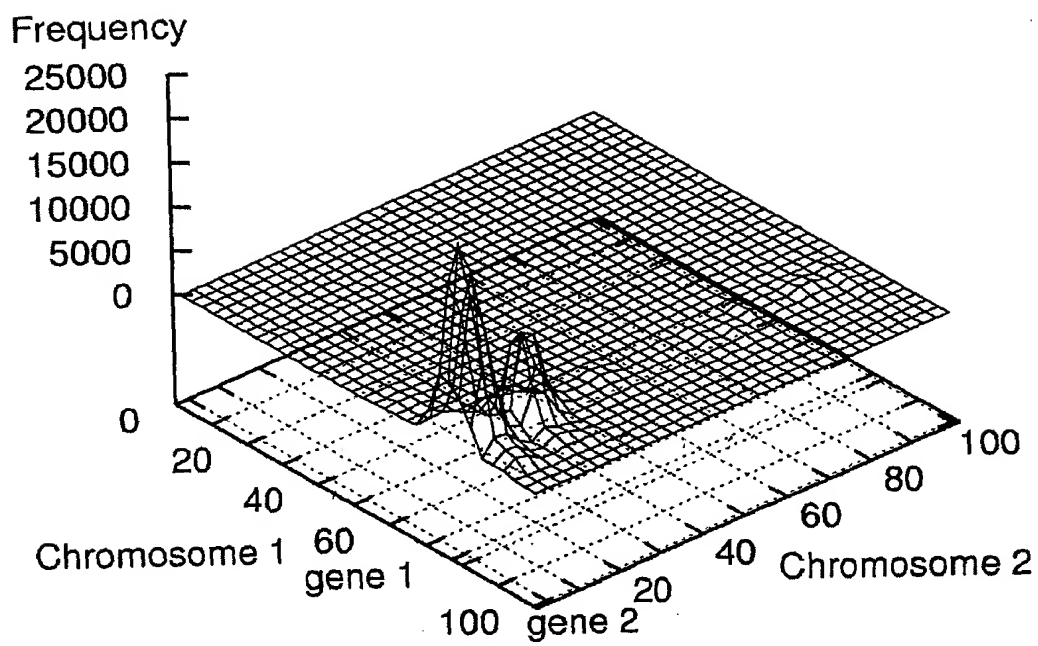


FIG. 6A

005959.000000

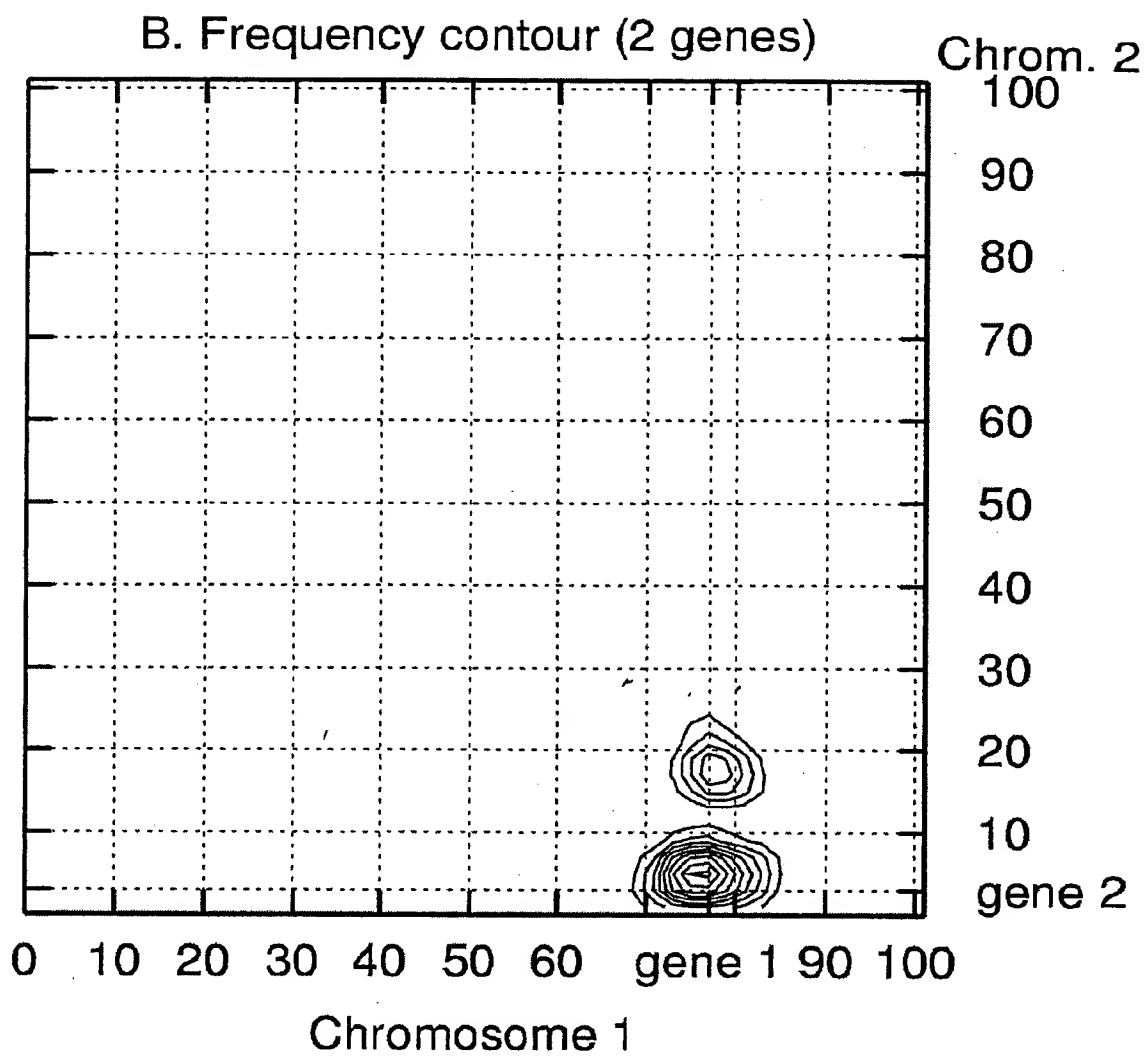


FIG. 6B

T08090" SE654860

C. Localization residuals (2 genes)

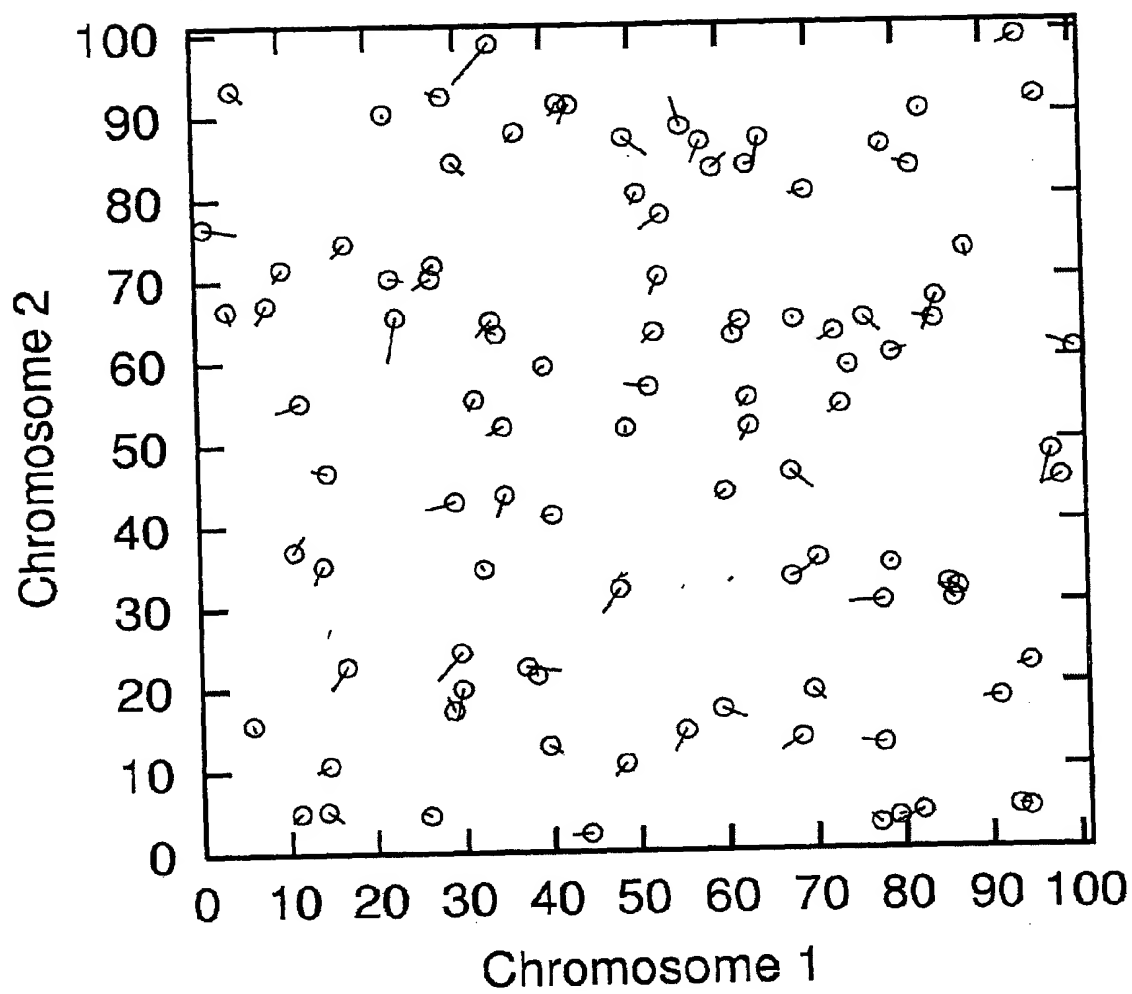


FIG. 6C

D. Prediction accuracy (2 genes)

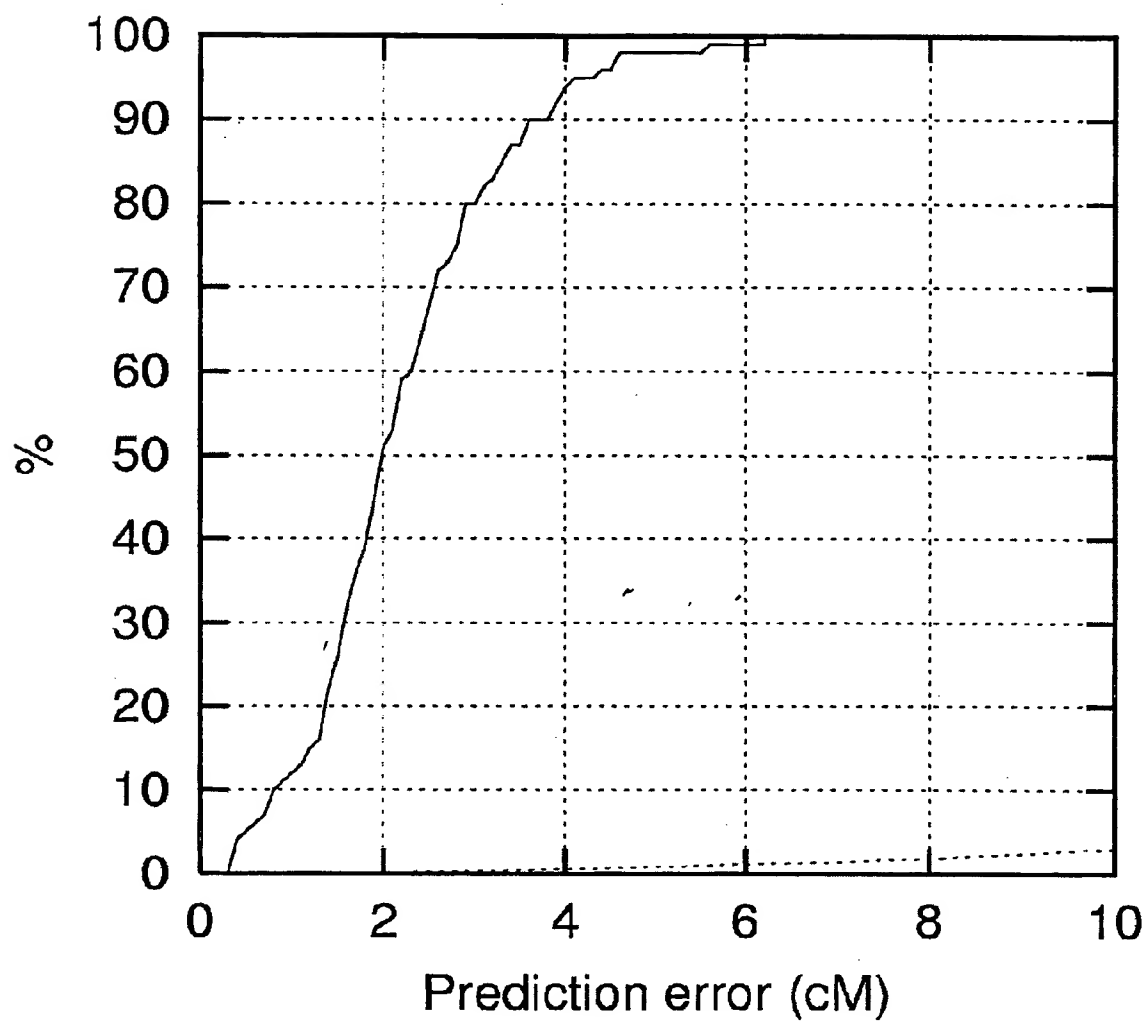


FIG. 6D

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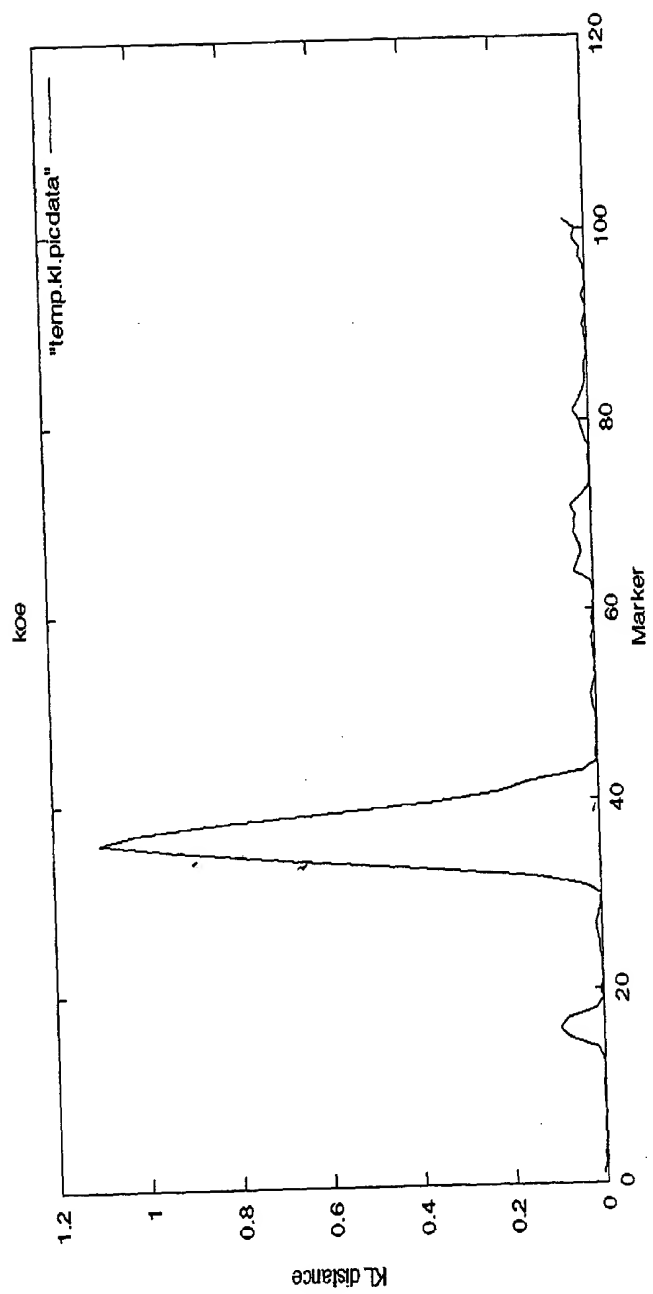


FIG. 7A

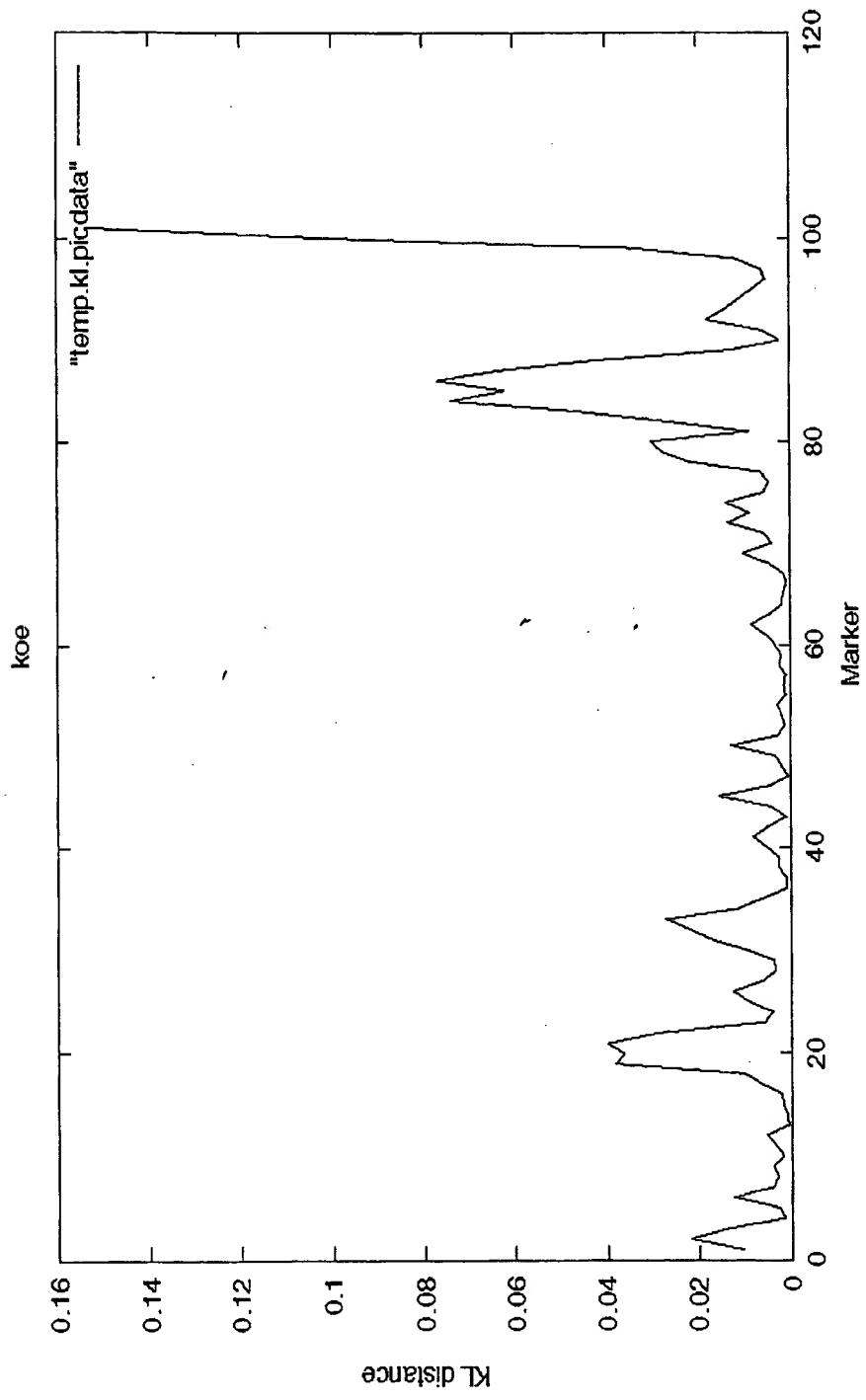


FIG. 7B